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BQ669630 AGENCOURT
BF338951 602036021
BMO44B16 60205683
BF20438 601866411
BE885725 601508937
BE296749 601175134
AV725513 AV725513
B1828125 601075385
B157614 602022587
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BC288435 602383404
BE87592 RCZ-FN009
BF20380 601868788
AIO05033 ouglb12.x
AW770546 h166c06.x
BC873035 601448124
BF872035 601448124
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BM313609 ig72h03.y
AA701598 zi34h07.s
A1127789 gc32c02.x
AL700814 DKF2p686H
AV667139 AV667139
BG927600 HNC49-1-E
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A1095556 qb19f04.x
A1127822 qc36f02.x
BF443234 260654 MA
AN015855 UI-H-BIO-
BM454007 AGENCOURT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:4122401C04:beta-site APP cleaving enzyme, full houses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                AL570757 AL570757
BF057767 7K53e11.x
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BE799078 601588381
AI857994 wj69a09.x
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (strain:C57BL/6J) 16 days embryo head cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:4122401C04.
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High-efficiency full-length cDNA cloning
Weth- Enzymol. 303, 19-44 (1999)
99279253
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BQ637035
BE872035
BF439471
BE793449
BM313609
                                                                                    BQ669630
BF338951
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BE885725
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AV725513
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BG288435
BE837592
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AL700814
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AI095556
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HTC; CAP trapper.
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AUTHORS
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JOURNAL
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AF150387 AF150387
AK014390 Mus muscu
BO94536 AGENCOURT
BO018588 UI H-DH1-
B1084083 602869445
                                                                                                                                        (without alignments)
11253.661 Million cell updates/sec
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                                                                                                                                                                                                                              Description
                                                                                                                   8, 2003, 18:08:33 ; Search time 2979 Seconds
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              5.1.6
Compugen Ltd.
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                GenCore version
Copyright (c) 1993 - 2003
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Gapop 10.0 , Gapext 1.0
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Minimum DB s Maximum DB s

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Searched:

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1559.6 991.6 958.2 819.6 746

426459

Score

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Result

after 3'

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/codon_start=1
/pucation_id="inab29370.1"
/db_xref="inab29370.1"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="16 days embryo"
1. 3859
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data source:MGD, source key:MGI:1346542, evidence:ISS
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selected before cloning. Vector: a modified pBluescript bulk excision from Lambda FLC I. Cloning sites, 5' end:
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87.5%; Pred. No. 2.1e-238;
iive 0; Mismatches 244;
                                                                                                                                                                                                                           /strain="C57BL/6J"
/db_xref="FANTOM_DB:4122401C04"
/db_xref="RAD:MGI:1896726"
/db_xref="taxon:10090"
/clone="4122401C04"
                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                   Location/Qualifiers
                                                                               end: BamHI. Host: DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="Bace"
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Best Local Similarity 87.5
Matches 1798; Conservative
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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Best Local Similarity 97.4%; Pred. No. 4.6e-148; Matches 1093; Conservative 0; Mismatches 19; Indels 10; Gaps 8; 712 GAGGTATCGACCACTGGGGAGGAGCACTCTGGTATACACCCATCGGGGAG 771	772 TGGTATTATGAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGAC 831	21 IOCAAGAAAGTGTTTGAAGCTGCAGTCAATCCATCAAGGCAGCTCCTCCACGGAGAAG 92 CCCAAGAAAGTGTTTGAAGCTGCAGTCAATCCATCAAGGCAGCTCCTCCACGGAGAAG 1	952 TTCCTGATGGTTTCTGGTTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGACCACCCCT 1011 	1012 IGGAACAITITCCCAGICATCTCACTCTACCTAATGGGIGAGGITACCAACCACCCTTC 1071 	1072 GGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAA 1131 	1132 GACGACTGTTACAAGTTTGCCATCTCACGGCACCGGGCACTGTTATGGGAGCTGTT 1191 	1192 ATCATGGAGGGCTTCTA-CGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGT 1250 	1251 CAGCGCTTGCCATGTGCACGATGAGTTCAGGACGGCAGGGGTGGAAGGCCCTTTTGTCAC 1310 	1311 CTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAG	1371 CATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCCCCTCTGCTCATGGT 1430	1431 GTGTCAG-TGGCGCTGCCTCCGCTGCCTGCCAGCAGCATGATGACTTTGCTGATGACA 1489 	1490 TCTCCCTGCTGAAGTGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACC 1549 	1550 TCCGTGGTTCACTTTGGTCACAAGTAGGACACAGATGGCACCTGTGGCCAGAGCACCT 1609 	1610 CAGGACCTCCCCACCACCAATGCCTCTGCCTTGATGGAGAAAGGCTGGCAAG 1669 	1670 GTGGGTTCCAGGGACTGTACTGTAGGAAACAGAAAGAGAAGAAGAACACTCTGCTG 1729 	30 GCGGGAATACTCTTGGT

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Kato, H., Kawai, J., Kojima, Y., Kondo, H., Kouda, M., Koya, S.,
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,
Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Schrim, L., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, F.,
Tanaka, T., Tejima, Y., Toya, T., Yamanuka, I.,
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AVIMEGFYVVFDRARKIGFRAYSAGHVHDEFRTAAVEGFFYTAADMEDCGYNIPQTDES
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1. .2503
                                                                                                                                                                                                                                                                                               Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                             Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
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/organism="Mus musculus"
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BQ018588 1747 bp mRNA linear EST 27-MAR-2002 UI-H-DH1-awu-c-12-0-UI.sl NCI_CGAP_DH1 Homo sapiens cDNA clone IMAGE:5823683 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1384 AIGGCIGCCATCIGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGC 1443
481 AIGGCIGCCATCIGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGC 540
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                                                                                                                          61 TTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGACACCACCCCTTGGAACATTTC
                                                                                                                                                                          CITCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTAC
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                                                          ITIGAAGCIGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGGT
             Gaps
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0; Mismatches
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Best Local Similarity 96.8%;
Matches 864; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ949536 . 913 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8733256 NIH_MGC_101 Homo sapiens CDNA clone IMAGE:6454803
                                   1020 TTCTGGTGGCAGGAATATCCTTAGACACCACAAACTTGAGT-TGGAAATTTTGCTGCTTG 1078
                                                                                     1841
                                                                                                                                                                              1138 TTATGTC---CTTCCAGAAGTACTGGCGTCATACTCAGGCTACC-CGGCATGTGTCCCTG 1193
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                  CICTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTG 1781
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Bukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 913)
1 (bases 1 to 913)
1 (bases 1 to 914)
Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                    1079 AAGCTTCAGCCCTGACCCTCTGCCAGCA-TCCTTTAGAGTCTCCAACCTAAAGTATTCT
                                                                                                                                                                                                                                 1194 TGGTACCCTGGCAGAGAAAGGCCAAATC-TCATTCCCTGCTGGCCAAAGTCAGCAGAAGA
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                                                                                     AAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAAACTATTCT
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2632 row: h column: 04
High quality sequence stop: 613.
High quality sequence stop: 613.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="epidermoid carcinoma, cell line"
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602869445F1 NIH_MGC_102 bp mRNA linear EST 20-JUN-2001 mRNA sequence.
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/clone="ltaxon:9606"
/clone=lib="NHH_WGC_103"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="bulb0 (phage-resistant).
/note="Organ: salivary gland; Vector: poTB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dT priming.
Site_2: EcoR1; cDNA made by oligo-dT priming.
Site_2: adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1059)
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CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1820 row: j column: 11
High quality sequence stop: 794.
I. 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 CCCTCCCCACCACCAATGCCTCTGCTTGATGGAGAAAAGGCTGGCAAAAGGGTGGG
                                                                                                                1735 AATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCCT
                                                                                                                                                                                                            267 GAACCITIGICACCATICCITIAAATICICCAACCCAAAGTATICITICITIAGTI
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  1615 CCCTCCCCACCCACCAATGCCTCTGCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGG
                                                                                           NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1. 717

/ Organism="Homo sapiens"
  / Ab_Arsef="texaon:9606"
  / Clone="IMAGE:582363"
  / Clone="IMAGE:582363"
  / Clone="IMAGE:582363"
  / Clone="Image:80163"
  / Lissue_type="Metastatic Chondrosarcoma"
  / Ab_host="DH10B (Life Technologies)"
  / Note="Organ: Lung; Vector: pT713-Pac (Pharmacia) with a modified polyllinker; Site_1: EcoR I; Site_2: Not I;
  // NCL CGAP_DH1 is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dTy18 tail. The sequence tag for this library is AGATCATTGC.

TAG_LIB-UI-H-DH1

TAG_IIS-UI-H-DH1

TAG_IIS-
         1494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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ACCESSION
VERSION
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SOURCE
ORGANISM
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BI084878/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (University of California, Berkeley) using ZAP-cDNA synchesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." 300 c 273 g 243 t
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                                                                                                                                                                                                            CTCACTCTACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCA
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                                                                                             852 CAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGC
                                                                           Gaps
                                                                           14;
                                                      Length 1059;
                                                        Score 740.6; DB 13; Length
Pred. No. 3e-108;
); Mismatches 54; Indels
                                                                           0;
                                                          35.8%;
92.5%;
                                                                            Conservative
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                                                                     Local
                               BASE COUNT
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="htms:10394"
/clone="htms:10394"
/clone="htms:10394"
/clone="htm:10394"
/clone="htm:10394"
/clone="build carcinoma, cell line"
/lab.host="bh108 (phage-resistant)"
/note="organ: salivary gland; Vector: porB7; Site_1: XhoI;
Site_2: Ecogn: cloned into EcoRT/XhoI sites using the
Directionally cloned into EcoRT/XhoI sites using the
following 5' dadptor: GGCGAG(G). Library constructed
by Ling Hong: int (adaptor: GGCGAG(G). Library constructed
by Ling Hong: int (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
1 others
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BIO84878 865 bp mRNA linear EST 20-JUN-2001
602869445T1 NIH_MGC_102.Homo sapiens CDNA clone IMAGE:5013994 3',
                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1168 ACGGGCACTGTTATGGGAG-CTGTTATCATGGAGGGCTTCTACGTTGTCTTTGATCGGGC
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                                                                                                                                                                                          Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 865) MIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1820 row: j column: 11
High quality sequence start: 18
High quality sequence start: 18
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                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                            BI084878.1 GI:14503208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      810; Conservative
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                                                              mRNA sequence.
BI084878
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904 bp mRNA linear EST 21-JUL-2000 601237528F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609631 5', mRNA sequence.
            /tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Preast: Vector: pCMV-SPORT6, Site_1: NotI;
Site_2: SAli; cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
full-length clones and constructed by Life Technologies.
Note: this is a NH_MGC Library."
221 c 197 g 171 t 2 others
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                                                                                                                                                                  Length 761;
                                                                                                                                                                                                  Indels
                                                                                                                                                                    DB 13;
                                                                                                                                                               Score 713.8; DB 13.
Pred. No. 6.3e-104;
0; Mismatches 4;
                                                                                                                                                                34.5%;
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1 (basea 1 to 761)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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BM016288 BM016288.1 GI:16530642
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388
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                                                                         506 GCAGCATGATGATTGCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGA
                                                                                                                       AGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACAC
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plate: LLAM12068 row: h column:
High quality sequence stop: 728.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5418687"
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GCCAAAGTCA 19
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1406

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//issue_type="placenta"
//ote="Vector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
enriched into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
60 thers
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                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 700)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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                                                                                                                                                                      601 GACAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTT
1287 AGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACA
                                                                                                                                                                                                                                  1347 GACAGATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCTCTT
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BP 191 91006 EVRY cedex - France
Email: seqrefêgenoscope cns.fr, Web : www.genoscope.cns.fr.
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Pred. No. 6.5e-100;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODIO22KF22"
/clone_lib="LTI_NFL006_PL2"
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99.3%;
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nes 688; Conservative
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VERSION .
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                                                                                                                                                                        ALL Unpublished (1999)

ALL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location-Inb-"NIH_MGC_44"

//lob-host="BullOb (phage-resistant)"

//lob-host="BullOb 
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Pred. No. 3.2e-100;
0; Mismatches 8; Indels 6;
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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98.1%;
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Anote—"Overcor: p7773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " a 177 c 190 g 176 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1666 CAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAAGAAGAAGAAGCACTCT 1725
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                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 718;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                           /clone="IMAGE:3479156"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                  32.9%; Score 681.4; DB 12; 99.3%; Pred. No. 8.9e-99; Naismatches 2;
                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
 ity sequence stop: 4
Location/Qualifiers
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
                                                                                                                                                                                                                                                 1609
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                                                                                                              1430 TGTGTCAGTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACA 1489
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 718)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 5e-95;
); Mismatches
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/db_xref="taxon:9606"
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99.4%;
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Best Local Similarity 99.4
Matches 681; Conservative
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE=0275949"
/clone_inb="NHE_MGC_102"
/tissue_type="*epidermoid carcinoma, cell line"
/tissue_type="*epidermoid carcinoma, cell line"
/lab_host="BHIOB (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into ECORIX/XhoI sites using the following 5' adaptor: GGGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NHE_MGC Library." (Life 2 others)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1424
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                                 AGENCOURT_8354446 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275949 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium.(LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2459 row: o column: 22
High quality sequence stop: 506.
Location/Qualifiers
rce
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 945)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 6.5e-98;
0; Mismatches 6; Indels 1:
                                                                                                                                BQ669630.1 GI:21780464
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Best Local Similarity 99.0%;
Matches 689; Conservative
                                                                                                                                                                                          Homo sapiens
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AUTHORS
TITLE
JOURNAL
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                                                                                                                   ACCESSION
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KEYWORDS
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                                                          1905 TACCCT-GGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGG 1963
1845 ITTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCTGTGG 1904
                                                                                                                                                                                                                                                              /dD_ACTE_ cazar_svvv
/clone="IMAGE:4184140"
/clone_lib="NCI_CGAP_Brn64"
/tissue_type="glibolastoma with EGFR amplification"
/lab_host="NH10B (Tl phage resistant)"
/note="organ: brain; Vector: pCWV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/note="Organ: prostate; Vector: pOTB7; Site_1: XhOI; Site_2: ECORI; CDNA made by olign-dT priming.

Directionally cloned into ECORI/XhOI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript IT RT (Life Technologies).

Note: this is a NIH_MGC Library."
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/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
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                 21
                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
               Plate: LLCM1943 row: f column:
High quality sequence stop: 696.
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llarity 96.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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Tissue Procurement: DCTD/DTP
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/lab.host="DHIOB (phage-resistant)" /
/lab.host="DHIOB (phage-resistant)" /
/note="Yorgan: muscle, Vector: porB7; Site_1: EcoRI; /
Site_2: Xhoi; Condan: muscle, Vector: porB7; Site_1: EcoRI; /
Site_2: Xhoi; Condan: muscle, Vector: porB7; Site_1: EcoRI; /
Directionally cloned into EcoRI/Xhoi sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500pp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGGTTTCTGGCTAGGAGAGCAGCTGGTGTGGCAAGCAGGCACCACCCCTTGGAAC 1017
                                                                                                              BF204338 11near EST 06-NOV-2000 601866411F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4106858 5',
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                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM987 row: e column: 03
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                            cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/db_xref="taxon:9606"
/clone="IMAGE:4106858"
/clone_lib="NIH_MGC_17"
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Location/Qualifiers
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- 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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### TITLE OF INVENTION: ALCHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 29915/62801

CURRENT APPLICATION NUMBER: US/09/548,372D

CURRENT FILING DATE: 1000-04-12

PRIOR FILING DATE: 1999-09-23

SAFURMER OF SEQ ID NOS: 73

SOFTWARE PARENTIN VINNER: US 60/101,594

NUMBER OF SEQ ID NOS: 73

LENGTH: 2070
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US-09-548-372D-40
US-09-548-367D-39
US-09-548-367D-39
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US-09-548-372D-3
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TES THEREFOR AND USE 3GGTTCCAG 1680 ||||||||||| 3GGTTCCAG 1680 3GGAATACT 1740 |||||||||||||||3 |GGAATACT 1740 CCCTGCTG 1500 |||||||||| ||CCCTGCTG 1500 

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Pred. No. 0;
                                                                                                                                                                                                                                       YSTEM: DOS
FastSEQ for Windows Version
                                                                                                                                                                                                                                                                 JMBER: US/09/009,191
20-JAN-1998
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9701684.4
FILING DATE: 28-JAN-1997
ATTONEX/AGENT INFORMATION:
NAME: PRESTIA, PAUL. F
REGISTRATION NUMBER: 23,031
                                             Sequence 1, Application US/09009191 Patent No. 6319689 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.2%;
                                                                           APPLICANT: POWELL, DAVID
APPLICANT: GHARMAN, CONRAD
APPLICANT: MURPHY, KAY
APPLICANT: SMITH, TRUDI
TITLE OF INVENTION: ASP2
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATHER & PRESTI
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                             COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DOS
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LENGTH: 2541 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 99.5
Matches 2049; Conservative
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APPLICATION NUMBER: US
FILING DATE: 20-JAN-19
CLASSIFICATION:
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                    Score 1887.2;
Pred. No. 0;
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                            CGCTGCCTCCGCTGCCTGCGCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG
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JUNEAU LINCORTAILON:

TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRET

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 29915/62801

CURRENT APPLICATION NUMBER: US/09/548,372D

CURRENT FILING DATE: 1909-00-23

PRIOR FILING DATE: 1999-00-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-23

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 73

SOFTWARE: PATENTION NUMBER: US 60/101,594

NUMBER OF SEQ ID NOS: 73

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 5

FENDOR FILING DATE: 1998-09-24
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ORGANISM: HOMO
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                                              SECRETASE,
                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALCHEINER'S DISEASE SECRE'
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR APPLICATION NUMBER: US 99/404,133
PRIOR APPLICATION NUMBER: US 99/404,133
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 73
SEQ ID NO 5
SEQ ID NO 5
SEQ ID NO 5
SEQ ID NO 5
                                                                                                                                                                                                                                                         91.2%; Score 1887.2;
96.2%; Pred. No. 0;
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         Sequence 5, Application
Patent No. 6440698
                                                                                                                                                                                                                                                                     Similarity
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Best Local Simil
Matches 1974; (
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                   TIGICCACCATICCITIAAAITCICCAACCCAAAGIAITCITICITIGITICAGAA
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APPLICATION NUMBER: US/09/009,191
FILING DATE: 20-JAN-1998
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APPLICATION NUMBER: UK 9701684.4
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09009191
Patent No. 6319689
GENERAL INFORMATION:
APPLICANT: POWELL, DAVID
APPLICANT: CHAPMAN, CONRAD
APPLICANT: MURPHY, RAY
APPLICANT: SMITH, TRUDI
TITLE OF INVENTION: ASP2
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
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STREET: P.O. BOX 980
CITY: VALLEY FORGE
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TELEPHONE: 610-407-0700
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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REGISTRATION NUMBER: 23,
REFERENCE/DOCKET NUMBER:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Query M Best Lo Matches	/ Match Local Similarity 98.8%; Pred. No. 0; nes 1867; Conservative 0; Mismatches 21; Indels 1; Gaps 1;	1192
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Db Qy	21 TTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGTGGG 4 52 GCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGAGGAGGATGATCATT 7 11111111111111111111111111111111111	OY 1731 CGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTTGCT
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දි	89	QY 1911 GCCAGAGAGACCAAGCTTGTTCCCTGCCGAAAGTCAGTAGGAGAGGATGCACA 1970. 
oy Oy	TGCAAGGAGTACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTGGTTTG 7 CCCAAGAAAAGTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAG 9	OY 1971 GTTTGCTATTTGCTTTACAGACAGGGACTGTATAACAAGCCTAACATTGGTGCAAAGAT 2030 
oy .	721 CCCAAGAAAGTUTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCTCCACGGGAAAG 700 952 TTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGGTGCTGGCAAGCAGCACCCCCT 1011	Qy 2031 TGCCTCTTGAATTAAAAAAAAAAAA 2059 
Qy Db	1012 TGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCA	RESULT 7 US-09-548-372D-7 ; Sequence 7, Application US/09548372D ; Patent No. 6420534
Qy Db	1072 CGCATCACCATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCCACGTCCCAA 1131	; GENERAL INFORMATION: ; APPLICANT: GUNENY ET AL. ; TITLE OF INVENTION: ALCHEMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE ; TITLE OF INVENTION: THEREOF
Qy Db	1132 GACGACTGTTACAAGTTTGCCATCTCACAGTCATCCACGGCACTGTTATGGGAGCTGTT 1191 	; FILE REFERENCE: 29915/62801 ; CURRENT APPLICATION NUMBER: US/09/548,372D ; CURRENT FILING DATE: 2000-04-12 ; PRIOR APPLICATION NUMBER: US 60/155,493

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PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
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PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR PILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PATENTIN VERSION 3.1
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Qy 421 CIGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGC	QY 481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 5	OY 541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACCCTGGAGCCTTTCTTGACTCT 6	OY 601 CTGGTAAAGCAGACCCACGTTCCCAACCTTTCTCCCTGCACCTTTGTGGTGCTGCTTTC 6 11111   1111111   1111111   11111111   111111	OY 661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGAGCATGATCATTGGAGGTATC 7	QY 721 GACCACTGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGGGTGGTATTAT	Oy 781 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 84	Qy 841 TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA	QY 901 GTGTTTGAAGCTGCAGTCATCATCAAGCCAGCTCCTCCACGGAGAAGTTCCCTGAT	QY 961 GGTTTCTGGCTAGGAGGAGCTGGTGTGCTGGCAAGCAGGCACCCCCTTGGAACATT	OY 1021 TICCCAGICATCICACITACCIAATGGGGGAGGTTACCAACCAGICCITCCGCAICACC	OY 1081 ATCCTTCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCAGGTCCCAAGACGGTTTTTTTT	OY 1141 TACAAGTTTGCCATCTCACAGTCACGGGCACTGTTATGGGAGCTGTTATCATGGAG	OY 1201 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC	QY 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG	Qy 1321 GAAGACTGTGGCTACAATTCCACAGACAGATGAGTCAACCTCATGACCATAGCCTAT	Qy 1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCTCATGGTGTGTGT	Oy 1441 CGCTGCCTCCGCTGCGCCAGCACGATGATGACTTTGCTGACATCTCCCTGCTG
CACAGTTTGCTA 1	AAGGCCAATC-TCATTCCTGCTGCTGCTAAGTCAGCAGAAGAAGGTGAAGTTTGCCA 1970 TTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTT 2031 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	Db 1971 GTTGCTTTAGTGATAGGGACTGCAGACTCAAGCCT-ACACTGGTACAAGACTGCGTCTT 2029  Oy 2039 GAATTAAAAAAAA 2052  IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 2030 GAGATAAACAAGAA 2043 RESULT 8	ഗയമജ		CURRENT APPLICATION NUMBER: US/09/548,367D CURRENT FILING DATE: 2000-04-12 PRIOR APPLICATION UNMER: US 60/155,493 PRIOR FILING DATE: 1999-09-23	PRIOR APPLICATION NUMBER: US 09/404,133 PROR FILING DATE: 1999-09-23 PRIOR APPLICATION NUMBER: PCT/US99/20881 PRIOR FILING DATE: 1999-09-29		SEQ ID NO LENGTH: TYPE: DNA ORGANISM	75.0%; Score 1552.4; DB 4; Length 2043; ilarity 87.6%; Pred. No. 0;	0; Conservative 0; Mismatches 241; Indels 13; Gaps Argecceaegcccreccrecrecrecres argecceaegcccreccrecrecrecres [	ATGCCCCAGCGCTGCACTGCTCCTGCTATGGGTGGGCTCGGGAATGCTGCCTGC	61 GGAACCCATCTCGGCATCCGGCTGCCCCTTCGCAGCGGCTGGGGCCACCCCTGGGC  121 CTGCGGCTGCCCCGGGAGACCGACGAGAGACCCGAGGACCGGGCGGG	121 CTGAGGCTGCCCGGGAGACTGACGAGGAATCGGAGGAGCCTGGCCGGAGAGAGGCTTT 1 181 GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 2	ACC 2 GCA 3	GCA 30 ACA 36 	Db 301 GTGGGGGCTGCCCCACACCCTTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA 360 Qy 361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAA 420

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361   TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAGTGGGAAGGGGGG   420	601 CTG 61 CCC 61 CCC 721 GAC 901 GTC 901 GTC 901 GTC 1021 TTC 1021 TTC 1081 ATC 1141 TAC 1141 TAC 1201 GG 1201 GG 1201 GG 1201 GG 1201 GG 1201 GG 1321 GAC 1321	s-09-548-372D-31 Sequence 31, Application US/09548372D Patent No. 6420534
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APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
TITLE OF INVENTION: THEREFOF
FILE REFERENCE: 29915/6280H
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 2000-04-12
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                            GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCCATCCGGCGGGAGTGGTATTAT
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PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
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                   TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND UTILE OF INVENTION: THEREOF TITLE OF INVENTION NUMBER: US/09/548,372D CURRENT APPLICATION NUMBER: US 66/155,493 PRIOR PELIOR DATE: 1999-09-23 PRIOR FILING DATE: 1999-09-23 PRIOR FILING DATE: 1999-09-23 PRIOR FILING DATE: 1999-09-23 PRIOR FILING DATE: 1999-09-24 NUMBER: US 66/101,594 PRIOR FILING DATE: 1999-09-24 NUMBER: OF SEQ ID NOS: 73
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LENGTH: 1380
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llarity 100.0%; Pred. No. 9.9e-310;
Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
TITLE OF INVENTION: ALZHEIMER'S DISEASE SEG TITLE OF INVENTION: THEREOF FILE REFERENCE: 29915/62801
CURRENT FILING DATE: 2000-04-12
PRIOR PAPLICATION NUMBER: US 60/155,493
PRIOR PILING DATE: 1999-09-23
PRIOR FILING DATE: 1998-09-24
NUMBER SEQ ID NOST: 73
SOFTWARE: PATCHION NUMBER: US 60/101,594
NUMBER: PECOL ID NOS: 73
SOFTWARE: PATCHION NUMBER: US 60/101,594
NUMBER: PATCHION OF SEQ ID NOS: 73
SOFTWARE: PATCHION NUMBER: 1998-09-24
NUMBER: PATCHION NUMBER: US 60/101,594
SEQ ID NOS: 73
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APPLICANT GUINEY TAL.
APPLICANT GUINEY TAL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRET
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 29915/6280H
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR PILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 21 US/09548367D 663 ŏ g

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Db 541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACAGCCTTGAGCCTTTGTTGACTCT 600	601 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC 66	QY         661 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGAGCATGATCATTGGAGGTATC 720           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 781 GAGGTCATCATTGTGGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 840 	QY 841 TACAACTATGACAATGTGGACACGGCACCACCAACTTGCCCAAGAAA 900 	QY 901 GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCTCCTCCACGAGAAGTTCCCTGAT 960 	OY         961 GGTTTCTGGCTAGGAGAGCAGCTGGTGGCAGCAGCAGCCCTTGGAACATT 1020           DD         961 GGTTTCTGGCTAGGAGCAGCTGGTGTGCTGGCAAGCAGCACCCCTTGGAACATT 1020	QY 1021 TICCCAGICATCICACTAACTAATGGGIGAGGITACCAACCAGICCTTCCGCATCAC 1080	OY         1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140           Db         1081 ATCCTTCCGCAGTAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140	OY 1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGG 1200	QY 1201 GGCTTCTACGTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260	OY 1261 CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAGGCCCTTTGCACCTTGGACATG 1320	OY 1321 GAAGACTGTGGCTACAACATTCCACAGACAGTGAGTCAACCCTCATGACCATT 1380	Oy 1381 GTCATGGCTGCCATCTGCGCCTCTTCATGCTCTCTCTGCTCTGGTGTGTGT	OY 1441 CGCTGCCTGCTGCGCGCGGCAGGATGACTTTGCTGATGACATCTCCCTGCTG 1500   11111111111111111111111111111111	QY 1501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACCTCGTGGTTCA 1560	QY     1561 CTTTGGTCACAAGTAGGACACACAGATGGCACCTGTGGCCAGACCCTCC 1620       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 1621 CCACCCACCAAATGCCTCTGCTCTGATGGAAAAGGTAAAAGGCTGGCAAGGTGGGTTCCAG 1680
Db 1981 TGCTTTAGAGACAGGGACTGTATAACAAGCCTAACATGGTGCAAAGATTGCCTCTTGA 2040		RESULT 2 AX378015 LOCUS LOCUS DEFINITION Sequence 1 from Patent W00206306. ACCESSION AX378015 VERSION AX378015 GI:19574050	OURGE human.  ORGANISM Homo sapiens  ORGANISM Homo sapiens  Elekaryota; Metazoa; Chordata; Craniata; Vertebrata; E	CE 1 RS Yan, R., Tomasselli, A.G., Gurney, M.E., Emmc and Heinrikson, R.L.	JULE SUBSIDERS and ASSAYS LOF _900'secretase activity JOURNAL Patent: WO 0206306-A 1 24-JAN-2002; FRATURES LOCATION/Qualifiers	i i	Query Match 100.0%; Score 2070; DB 6; Length 2070; Best Local Similarity 100.0%; Préd. No. 0; Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ATGCCCCAAGCCCTGCCCTGCTCTGCTGGATGGCGCGGGAGTGCTGCTGCCCAC 60  ATGCCCCAAGCCCTGCCTGCTCTTGTTGTGATGGCGCGGGAGTGCTGCTGCCTGC	61 GGCACCCAGCACGCATCCGGCTGCCCTGCGCGCCTGGGGGGCCCCCCTGGGG 1	FTT 18	181 GTGGAGATGGTGGACAACCTGAGGGCCAAGTCGGGCCAGGCCTACTACGTGGAGATGACC 24 181 GTGGAGATGGTGGACAACTCTGAGGCCAAGTCGAGGCTAATACGTGGAATGACC 24	GTGGGCAGCCCCCGCAGAGCGCTCAACATCCTGGTGGATACAGGCAGCAGCAGTTTGCA 30 	SCACA 3	366AG 42	421 CTGGGCACCGACCGTGCTACCCCATGGCCCCAACGTCACGCGTGCCCAACATT 48	481 GCTGCCATCACTGAATCAGACTCTTCATCAACGGCTCCAACTGGGAAGGCATCTG 54	401 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGGCTCCTGGAGGCTTTGA

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11 aspartyl protease 2 mRNA, complete cds.
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                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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19n,R., Bienkowski,M.J., Shuck,M.E., Miao,H., Tory,M.C.,
Pauley,A.M., Brashler,J.R., Stratman,N.C., Mathews,W.R., Buhl,A
Carter,D.B., Tomasselli,A.G., Parodi,L.A., Heinrikson,R.L. and
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Submitted (29-OCT-1999) Genomics Research, Pharmacia&Upjo Henrietta, (Ralmazoo, MI 49007, USA

Location/Qualifiers

1. 2070

/ Organism="Homo sapiens"

/ Ab_xref="taxon:9606"

/ Chromosome="11"

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/protein_id="AAF17079.1"
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,M., Dovey,H.F., Frigon,N., Hong,J.,
,K., Jewett,N., Keim,P., Knops,J., Lieberburg,I.,
H., Tatsuno,G., Tung,J., Schenk,D., Seubert,P.,
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/product="APP beta-secretase"
/product="APP beta-secretase"
/protein_id="APR1892.1"
/db_xref="G01445"
/db_xref="G115001445"
/translation="WAQALPWILLWWGAGVLPAHGTOHGIRLPLRSGLGGAPLGLRLP
RETDEEPEEPGRRGSFVEWVDNLRGKSGGGYYVEMTVGSPPOTLNILVOTGSSNRAVG
AAPHFEHRYYQFOLSSTYRDLRGYVYPTYGGKWEELGTDLVSIPHGPNVTWRNI
AATHESDKFFINGSNWEGILGLAYABIARPDDSLEPFPDSLVKQTHVPNLFSLQLCGA
GFPLNQOSEVLASVGGSMIIGGIDHSLYTGSLMYTPIREWYEVEVITVRPLNGQDLKM
DCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAG
TTPNNIFPYLSLYLKMGEVPNTROFRYRITILPQQYLRPVBDYATSQDDCYRFAISQSSTGT
VMANVIMEGFYVVFDRARKRIGFAAVSACHVHDEFRTAAVEGFFVTLDMEDCGYNIPQT
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                                                                    2 (bases 1 to 5878)
Basi,G.S., Power,M.D., Wang,S., Tatsuno,G., Fri
Hong,G., Keim,P., Anderson,J., Sinha,S. and MCC
Direct Submission
Submitted (03-NOV-1999) Gene Expression Group,
Pharmaceuticals, Inc., 800 Gateway Blvd., S. Sa
94080, USA
                       precursor
 Zhao, J.,
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6
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                                                                                                                                                    Location/Qualifiers

1. 5878

1. 5878

2. Organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="11"

/tissue_type="brain"

455. .1960

/function="cleaves APP at the be
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Pred. No. 0;
0; Mismatches
         John,V.
Purification and cloning of amyloid beta-secretase from human brain Nature 402 (6761), 537-540 (1999)
Suomensaari, S., Wang, S., Walker, D.,
                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.2%;
ilarity 99.8%;
Conservative
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Matches 2055; Conserv
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/gene="KIAA1149"
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                                                                                                                                                                                        /note="Start codon is not identified."
/tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
/dev_stage="adult"
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1510 c 1404 q 1406
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                                                                                                                                                                                                                              /product="KIAA1149
                                                                                                                                                                        /gene="KIAA1149"
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Direct Submission

Submitted (04-007-1999) Osamu Ohara, Kazusa DNA Research Institute,
Submitted (04-007-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
Fax:+81-438-52-3914, Sequence version replaced gi:6330044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAAG 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGGAGGATGCACAGTTTGCTATT 1980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Characterization of cDNA clones selected by the GeneMark analysis from size-fractionated cDNA libraries from human brain DNA Res. 6 (5), 329-336 (1999)
           AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 2014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                              CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCCAGAGCACCTCAGGACCCTCC
                                                                       GGACTGTACCTGTAGGAAACAGAAAAGAAGAAGAAGAAGCACTCTGCTGGCGGGAATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (sites)
Hirosawa,M., Nagase,T., Ishikawa,K., Kikuno,R., Nomura,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AB032975 S814 bp mRNA linear
Homo sapiens mRNA for KIAA1149 protein, partial cds.
AB032975
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/db_xref="taxon:9606"
/clone="fg04087"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens adult male brain
SK plus clone:fg04087.
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PN JP 2000060579-A/1
PD 29-FEB-2000
PP 28-TEB-2000
PP 28-GAN-1997 GB 9701684:4
PI 28-JAN-1997 GB 9701684:4
PI DAVID J POWERU, CONRAD G CHAPPUMAN, KAY MAFI, TRUDY S SMITH PRIZNIN 31/7088, A61K89/00, A61R39/395, A61K848/00, A61P25/28, A61P35/00, A61P
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Aspartate proteinase ASP2
Patent: JP 2000060579-A 1 29-FEB-2000;
SMITHKLINE BEECHAM CORP
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CC Topology: Linear;
FH Key Lo
FT source 1.
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Local Similarity 99.5%;
les 2049; Conservative
                                                      (bases 1 to 2541)
  JP 2000060579-iunidentified.
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1620 CCCACCACAANTCCTCTGCTTCATGGGAAAAGGTGGGATCCA   1611	Q7 D	Oy Db	Qy Db	cy Ga	QY	Qy Bp	da .	QY Db	Qy Db	QY Db	Qy Db	Q Q	Oy	O. D.	Qy Dp	λ <sub>O</sub>	QY	40	Oy
1620 CCCACCACAANTCCTCTGCTTCATGGGAAAAGGTGGGATCCA   1611	<u> </u>																		
	1620 CCCACCCACCAAATGCCTCTGCCTTGATGGAAAGGAAAAGGCTGGCAAGGTGGGTTCCA 167	1680 GGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAGAAGCACTCTGCTGGCGGGAATAC 173 	1740 TCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACC 179 	1800 TTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTTCT	1860 AGTACTGGCATCACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAAA 191	1920 GAGACCAAGCTIGTITCCCTGCTGGCCAAAGTCAGTAGGAGGATGCACAGITIGCTAT 197	1980 TTGCTTTAGAGACAGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG 203 	2040 AATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		AXO62111 GI:12540032	SM Homo sapiens Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleos	Manufalla; Lutherlaf, Frimates; Catafrini; Hominidae; H (bases 1 to 3252) Tang,J.J., Hong,L. and Ghosh,A.K. Inhibitors of mempsin 2 and use thereof	Oklahoma Medical Research Foundation (US); THE BOARD OF TRUSTEE OF THE UNIVERSITY OF ILLINOIS (US)  Location/Qualifiers		tch al Similarity 99.8%; Pred. No. 0; 2013: Conservative 0: Mismarches 5; Indels 0: Gans	40 GCGGGGTGCTGCCCACCACCACCACCATCCGGCTGCCCTGCGCACGGC 99 11	100 CTGGGGGGCGCCCCCTGGGGCTGCCCGGGGAGACCGACGACGACGAGGGGGGGG	160 CCCGCCGGAGGGCAGCTTTGTGAGAGATGGTGACACTGAGGGCAAACTGGGGCAACTTTGTGAGAGATGGTGAAACCTGAGGGGCAAGTCGGGGCAG	121 CCCGGCCGGAGGGCAGCTTTGTGGAGATGGTGGAGACAACCTGAGGGGCAAGTCGGGGGAG 1

BASE COUNT 804 a 863 c 811 g 771 t 3 others ORIGIN	Query Match 97.1%; Score 2010; DB 6; Length 3252; Best Local Similarity 99.8%; Pred. No. 0; Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	Qy         4.0 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACCGGCTGCCCCTGCGCGCGC	Oy 100 CTGGGGGGCCCCCCTGGGCTGCGGCTGCCGGGAGCACCGAGGAGGT59	QY         160 CCCGGCCGGGGGGCAGCTTGTGGAGATGGTGGACAAACCTGAGGGGCAAGTCGGGGCAG 219           111111111111111111111111111111111111	dy · 220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGCGCTCAACATCCTGGTGGAT 279	OY 280 ACAGGCAGCAGTAACTTTGCAGTGGTGCTGCCCCCCCCCTCCTGCATCGCTACTAC 339	Oy 340 CAGAGGCAÖCTGTCCAGCACATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACC 399 11111111111111111111111111111111111	QY         4.00 CAGGGCAAGTGGGAAGGGAAGTGGGCACCTGGTAAGCATCCCCCATGGCCCCAAC 459           1	0y 460 GTCACTGTGCGTGCCAACATTGCTGCCATCACTGAATCAGAAGTTCTTCATCAACGGC 519	OY 520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579	OY 580 CTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTTCTCCTG 639	Qy 640 CACCTITGTGGTGCTGGCTTCCCCTCAACCAGTGTGGAGGCTCTGTCGGAGGG 699	QY         700 AGCATGATCATTGGAGGTATCGACCACTCCCTGTACACGCAGTCTCTGGTATACACCC         759	QY 820 CTGAAAATGGACTGCAAGGAGTACAATGACAAGAGCATTGTGGACAGTGGCACCACC 879	Qy. 880 AACCTTGGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAATCCATCAAGGCAGCCTCC 939	QY         940 TCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAGCTGTGTGTG	QY 1000 GGCACCACCCTTGGAACATTTCCCAGTCATCTCACTTATGGGTGAGGTTACC 1059
Db 1261 CCTTTGCCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAG	1360 ACCCTCATGACCATAGCCTATGTCATGCCTGCCATCTGCGCCCTCTTCATGCTGCCAC	QY 1420 FGCCTCATGGTGTGTGAGTGGCGTGCCTCGGTGCGCGCGGCGAGCAGCAGCAGTGACTTT 1479	QY 1480 GCTGATGACATCTCCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCT 1539	QY 1540 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGCCACCTGTGGC 1599	1600 CAGAGCACCTCAGGACCTCCCCACCAAATGCCTCTGCCTTGATGGAGAAAA 1659 	QY 1660 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAGAA	QY 1720 CACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1779	OY 1780 TGAAACTTCAGCCCTGAACCTTTGTCCACATTCCTTTAAATTCTCCAACCCAAAGTATT 1839	QY 1840 CTTCTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1899	Qy 1900 TGTGGTACCCTGGCAGAGAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959 	QY 1960 GAGGATGCACAGTTTGCTATTTGCAGGACAGGGACTGTATAACAAGCCTAACATT 2019	2020 GGTGCAAAGATTGCCTCTTGAATTAAAAAAAAAA 2057 111111111111111111111111111111111111	RESULT 11 AX063201 LOCUS AX063201 3252 bp DNA linear PAT 24-JAN-2001 DEFINITION Sequence 1 from Patent W00100663. ACCESSION AX063201 VERSION AX063201 GT:12541045	S human ISM Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,	REFERENCE 1 (bases 1 to 3252) AUTHORS Tang, J. J. Lin, X. and Koelsch, G. TITLE Catalytically active recombinant memapsin and methods of use there	of JOURNAL Patent: WO 0100663-A 1 04-JAN-2001; Oklahoma Medical Research Foundation (US) FEATURES Location/Qualifiers	source 1. 3252 /organism="Homo sapiens" /db_xref="taxon:9606"

qq	961 GGGACCACCCCTTGGAACATTTTCCCAGTCATCTCACTTAACCTAATGGGTGACGTTACC 1020	1,00115	
λ O	0 AACCAGTCCTTCCGCATCACATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTG 1	DEFINITION ACCESSION VERSION KEYWORDS	Sequence 1 from Patent W002053594. AX472368
oy Db	10 GCCAGGTCCCAAGACGACTGTTACAAGTTTGCCATCTACAGGTCATCCAGGGCACTGTT	SOURCE	human.  M Homo sapiens Eukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Oy Db	1180 ATGGGAGCTGTTATCATGGAGGCCTTCTACGTTGTCTTGATCGGGCCCGAAACGAATT 1239 	REFERENCE AUTHORS TITLE JOURNAL	1 Ghosh,A.K., Koelsch,G. and Tang,J.J. Inhibitors of memapsin 2 and use thereof Patent: WO 02053594-A 1 11-JUL-2002,
Qy Db	1240 GGCTTTGCTGTCAGCGCTTGCCATGTGCAGGATGAGTTCAGGACGCGGGGGGGAGGG 1299 	FEATURES SOUR	ce
	1300 CCTTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAG	BASE COUNT ORIGIN	804
දු අ	1360 ACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGCCCCTCTTCATGCTGCTGCCTCT 1419	Query Match Best Local Matches 201	Query Match 97.1%; Score 2010; DB 6; Length 3252; Best Local Similarity 99.8%; Pred. No. 0; Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy Db	1420 TGCCTCANGGTGTCAGTGGCGCTGCCTGCCTGCGCCAGCAGCATGATGACTTT 1479	Oy Dp	40 GCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGC 99
Oy Db	1480 GCTGATGACATCTCCCTGCTGAAGTGAGGGCCCCATGGGCAGAAGATAGAGATTCCCCT 1539 	Oy Db	100 CTGGGGGCGCCCCCCTGGGGCTGCCGCGGGAGACCGAAGAGCCCGAGGAG 159
Oy Db	1540 GGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGACACACAGATGGCACCTGTGGC 1599 	Oy Dp	160 CCCGGCCGGAGGGCAGCTTTGTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAG 219 
Oy Db	1600 CAGAGCACCTCAGGACCCTCCCCACCACAATGCCTCTGCCTTGATGGAGAAGGAAAA 1659 	Qy Dp	220 GGCTACTACGTGGAGATGACCGTGGGCAGCCCCCGCAGACGCTCAACATCCTGGTGGAT 279
Oy Dp	1660 GGCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAAACAGAAAAGAGAAAGAA	. qa	280 ACAGGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCCCC
ò d	1720 CACTCTGCTGGGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGCT 1779 	Qy	340 CAGAGGAGCTGTCCAGCACATACCGGAACGTCCGGAAGGGTGTGTATGTGCCCTACACC 399 11111111111111111111111111111111111
Zo qa	1780 TGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATT 1839 	Qy	400 CAGGGCAAGTGGGAAGGGGAGCTGGGCACCTGGTAAGCATCCCCCATGGCCCCAAC 459 
Oy Db	1840 CITCITITCITACITICAGAAGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCC 1899 	QY	460 GTCACTGTGCGGCGAACATTGCTGCCATCACTGAATCAGAAGTTCTTCATCAACGGC 519 
Oy Db	1900 TGTGGTACCTGGCAGAGAAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA 1959 	QY	520 TCCAACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCC 579
Oy Dp	1960 GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT 2019 	Qy Dp	580 CTGGAGCCTTTCTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTG 639 [
O <sub>Y</sub> Db	2020 GGTGCAAAGATTGCCTGTTGAATTAAAAAAAAAA 2057 	Oy Db	640 CACCTTTGTGGTGCTGGCTTCCCCCTCAACCGGTCTGAAGTGCTGGCCTCTGTCGGAGGG 699 11
RESULT AX47236	12 8	Qy	700 AGCATGATCATTGGAGGTATCGACCACTGGCTGTACACAGGCAGTCTCTGGTATACACCC 759 

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SGTTNLRLPKKVFEAAVKSIRAASSTEKFPDGFWLGEQLVGWQAGTTPWNIFPVISLY
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FDRRARKRIGFAVSACHVHDEFFRAAVAGFFVTLDMEDCGYNIPQTDESTLMTIAYWA
AICALFMLPLCLMVCORRCLRCLRQQHDDFADDISLLK"

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                                                             CITCITITICITAGITITCAGAAGIACIGGCAICACACGCAGGIIACCITGGCGIGIGICCC
             TGTGGTACCCTGGCAGAGAAGAGCCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA
                                                                                                    GAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATT
                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele. Mammalia; Eutheria, Primates; Catarrhini, Hominidae; Homo. Lin, Cases 1 to 355.
Lin, X., Koelsch, G., Wu, S., Downs, D., Dashti, A. and Tang, J. Human aspartic protease memapsin 2 cleaves the beta-secretic of beta-amyloid precursor protein

Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1456-1460 (2000)
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et, Oklahoma City,
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Lin, X., Koelsch, G. and Tang, J.
Direct Submission
Submitted (28-OCT-1999) Protein Studies Prot
Besearch Foundation, 825 N.E. 13th Street, OFA
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/note="membrane-associated
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llarity 99.8%;
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Description	Human aspartyl pro Human aspartyl pro Human aspartyl pro Human cDNA encodin DNA encoding human Human aspartyl pro Human Asp-2(a) nuc Human aspartyl pro DNA clone pCEK Cl.
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New enzyme designated human aspartase useful in research into Alzheimer's Disease is capable of cleaving amyloid protein precursor at

Yan R;

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Gurney ME, Bienkowski MJ, Heinrikson RL,

WPI; 2000-303209/26. P-PSDB; AAY88425.

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Claim 

This sequence represents the human aspartyl protease 2 (Asp2) nucleotide sequence. The invention relates to a protease (e.g. Asp2) capable of cleaving the beta secretase site of amyloid precursor protein (APP). The protease contains a sequence encoding the amino acids sequence DTG and a sequence encoding DSG or DTG separated by 100-300 amino acids. When the paper causes an autosomal dominant form of Alzheimer's disease. APP localises to the cell surface membrane and have a single c'terminal transmembrane domain. Proteclytic processing of APP produces the amyloid beta protein, which is possibly very important in Alzheimer's disease, a vector containing the nucleotide sequence, and a cell line comprising the vector. Methods for screening for inhibitors of beta secretase activity are also given in the invention. The human aspartase protein and nucleotide sequences and the methods for identifying in to Alzheimer's disease. peptide beta amyloid produce English. 2; 183pp; Fig

BP; 476 A; 583 C; 562 G; 449 T; 0 other; Sequence 2070

ó 240 300 360 420 420 480 480 540 009 009 720 180 300 360 120 120 09 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCCAGGGCAAGTGGGAAGGGGAA TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGGTGCTGCTTC GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC GIGGGCAGCCCCCCCCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA GTGGGTGCTGCCCCCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA GGCACCCAGCACGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCCTGGGG DB 21; Length 2070; ö Indels ô larity 100.0%; Score 2070; 101.14y 100.0%; Pred. No. 0; Conservative 0; Mismatches Best Local Similarity Matches 2070; Conser 541 601 181 241 301 361 361 421 481 181 541 601 661 61 61 121 121 181 241 301 121 Query Match q Qγ pp 염 Db a ò δ ö óλ g ò Dp οy g ò a ò g ŏ

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The patent discloses human aspartyl protease 1 (hu-Aspl) or modified Aspl proteins which lack transmembrane domain or amino terminal domain or cytoplasmic domain and retains alpha-secretase activity and amyloid protein precursor (APP) processing activity. The proteins of the invention are useful for assaying hu-Aspl alpha-secretase activity, which in turn is useful for identifying modulators of hu-Aspl alpha-secretase activity, where modulators that increase hu-Aspl alpha-secretase activity, where modulators that increase thu-Aspl alpha-secretase activity are useful for treating Alzhaimer's disease (AD) which causes progressive dementia with consequent formation of amyloid plaques, neurofibrillary tangles, gliosis and neuronal loss. Hu-Aspl protease substrate is useful for assaying hu-Aspl proteolytic actioity, by contacting hu-Aspl protein with the substrate under activity. By contacting hu-Aspl protein with the substrate under activity. The present sequence is a cDNA encoding long form of human Aspl protein, designated as Aspl(a). Aspl gene is localised on chromosome 11q23.3-24.1.
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Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
                          AGACCAAGCTTGTTTCCCTGCTGCCCAAAGTCAGTAGGAGGATGCACAGTTTGCTATT
                                                                  GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGAG
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inhibitors of Asp2
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                                                                                                                                                     Human aspartyl protease 2a (Hu-Asp2a) cDNA.
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HEINRIKSON R L
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    GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCCATCCGGCGGGAGTGGTATTAT
                                         GAGGICATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG
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The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid precursor protein (APP) isoforms and their corresponding DNA molecules. Human aspartyl proteases can act as beta-secretase proteases useful for treating Alzheimer's disease. APP isoforms are useful for identifying modulators of amyloid-beta peptide production, for use in designing therapeutics for the treatment and prevention of Alzheimer's disease, dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis and neuronal loss. APP isoforms are also used in methods for identifying inhibitors and modulators of human Asp2 activity. The invention relates to a method for identifying agents that modulate the activity of human aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used as a means to screen in cellular assays for the inhibitors of beta- and gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in polymerase chain reactions (PCR). The probes are useful for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and Southern blots. The present cDNA sequence encodes human aspartyl protease 2 (Hu-Asp2), a 'long' form designated as (Hu-Asp2a). Hu-Asp 2 gene is

Sequence 2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other;

ö 120 120 180 180 240 240 300 300 360 360 420 420 480 540 900 900 099 720 720 9 09 GCCACCCAGCACGCCATCCGGCTGCCCCTGCGCGGCGCCTGGGGGGGCGCCCCCTGGGG GTGGGCAGCCCCCCCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA GTGGGTGCTGCCCCCCCCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG CTGGTAAAGCAGACCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGCTTC CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT GTGGAGATGGTGGACCACCTGAGGGGCAAGTCGGGGCCAGGGCTACTACGTGGAGATGACC TACCEGEACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG Gaps 2070; ; 22; Length Indels ; 0 DB 2070; No. 0; Mismatches 100.0%; Score 100.0%; Pred. ; 0 Conservative Best Local Similarity Matches 2070; Conserv 541 61 121 121 181 181 241 241 421 541 601 661 Query Match 61 301 301 361 361 421 481 481 601 661 ģ g ò Db g g qq δ qq ŏ Qγ q Ω g ŏ ò Qγ g ò δ g ŏ õ

1020 1020 1080 1080 1140 1200 1200 1260 1260 1320 1380 1380 1440 1440 1500 1500 1560 1560 1620 1680 1680 1800 780 900 960 GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGGGTGGTATTAT GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT GGTTTCTGGCTAGGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC CATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGG CGCTGCCTCCGCTGCCCTGCGCCAGCAGCATGACTTTGCTGATGACATCTCCCTGCTG AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC CCACCCACCAAAATGCCTCTGCCTTGATGGAGGAAAGGAAAAGGCTGGCAAGGTGGGTTCCAG GGACTGTACCTGTAGGAAACAGAAAAGAAGAAGAAGAAGCACTCTGCTGGCGGGAATACT GGACTGTACCTGTAGGAAACAGAAAAGAGAAAGAAGAAGCACTCTGCTGGCGGGAATACT 1141 1201 1321 1441 1501 1561 721 781 781 841 841 961 1021 1021 1081 1081 1201 1261 1261 1321 1381 1381 1441 1501 1561 1621 1621 1681 1681 1741 1741 721 901 901 961 qq δ g d g g g ΩÝ g Qγ q g Qγ qq δ g ŏ g à g ŏ δ ద ò QΥ οy Ω οp Qγ ò q δ g ŏ

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                                   GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGCCTGTGTGCTACCCTGGCAGAAG
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neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
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HEINRIKSON R L.
PARODI L A.
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Procease 2, lacking Asp2 transmembrane domain and retaining beta secretase activity of Asp2 useful for identifying inhibitors of Asp2 XX XX Claim 98; Fig 2; 185pp; English.

**Claim 98; Fig 2; 185pp; English.

**Crammalian aspartyl protease (Asp)2 protein, and where the polypeptide and transmembrane domain and the Asp2 protein, which lacks the Asp2 tronsmembrane domain and the Asp2 protein, and where the polypeptide and protein. The invention also details polynocleotides for the Asp2 protein and vectors expressing them, and a polypeptide (isoform of protein and vectors expressing them, and a polypeptide (isoform of amyloid protein precursor (APP) Comprising the amino acid sequence of an APP or its fragment containing an APP cleavage site recognizable by a campoxyl terminus of the amino acid sequence of the mammalian beta-secretase, and further comprising two lysine residues at the carboxyl terminus of the amino acid sequence of the mammalian APP or useful for treating Alzheimer's disease. APP is useful in methods for useful for treating Alzheimer's disease. APP is useful in methods for identifying inhibitors or modulators of human ASp2 activity and therapeutics for the treatment or prevention of Alzheimer's disease. APP comprising the APP-SW-beta-secretase peptide sequence (NLDA), which is assays relating the APP-SW-beta-secretase peptide sequence (NLDA), which crecombinantly expressing APP. Nucleic acids that hybridise to assays relating the Alzheimer's research. The expression vector is useful for detecting Hu-APP-SW-beta-secretase peptide sequence encodes are useful so probes or primers. The probes or primers and in Northern and Southern blots. The present sequence encodes human Asp2(a).
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aspartyl protease 2; Asp2; amyloid protein precursor; APP;
beta-secretase; Alzheimer's disease; ds.
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The invention relates to a novel purified polypeptide comprising a fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the Asp2 transmenbrane domain and the Asp2 protein, and where the polypeptide and the fragment retain the beta-secretase activity of the mammalian Asp2 protein. Also included is an isoform of amyloid protein precursor (APP) comprising the amino acid sequence of a APP or its fragment containing comprising the amino acid sequence of the mammalian APP or Isoform of the carboxyl terminus of the anino acid sequence of the mammalian APP or APP fragment. The polypeptides are used for assaying for modulators of beta-secretase activity, identifying agents that inhibit the APP processing activity of Asp2; and for reducing cellular production of anyloid beta (Abeta) from APP. Agents identifying agents that anyloid beta (Abeta) from APP. Agisase; and for identifying activity of Asp2; and for reducing cellular production of anyloid beta (Abeta) preptide production, for use in designing therapeutics for the treatment or prevention of Alzheimer's disease; and for identifying contains and assaying the activity of Asp2; and for modulators of amyloid-beta (Abeta) preptide production, for use in designing therapeutics for the treatment or prevention of Alzheimer's disease, probes and sprimers derived from Asp nucleic acid sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are useful for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and Southern blots. The present sequence represents the coding sequence of human Asp-2a used in the methods of the invention.
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The present invention relates to enzymes for cleaving the alphaseretase site of the amyloid precursor protein (APP) and methods of identifying those enzymes. The methods may be used to identify enzymes that may be used to cleave the alpha-secretase cleavage site of the APP protein. The enzymes may be used to treat or modulate the progress of Alzheimer's disease. The present sequence is human aspartyl protease (Asp) 2a cDMA. ASP 2a has beta-secretase protease activity. Asp2 gene is located on chromosome 11q23.3-24.1.
                                                                                                                                                                                                                                                                                                                                                                                                         CTGCGGCTGCCCCGGGAGACCGACGAGGAGCCCGAGGAGCCCGGAGGGGCAGCTTT
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                                                                                                                                                               Enzymes that cleave the alpha-secretase site of the amyloid protein, useful for the treatment of Alzheimer's disease -
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                                                                                                                                                                                            Example 2; Page 126-127; 189pp; English
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                                                                                           (PHAA ) PHARMACIA & UPJOHN CO
                                                 99WO-US20881.
99US-0416901.
99US-0169232.
                      2000WO-US26080
                                          99US-0155493
                                                                                                               Gurney M, Bienkowski MJ;
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                 WPI; 2001-290516/30.
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Best Local Similarity
Matches 2070; Conserv
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                                                 23-SEP-1999;
13-OCT-1999;
06-DEC-1999;
                      22-SEP-2000;
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                    CTTTGGTCACAAGTAGGACACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC
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/note= "Pre-pro-peptide"
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	1 GGGCTGGCCTATGCTGAATTGCCAGGCCTGACGACTCCTGGAGCCTTTGACTGTTTGACTCT	CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGCTTGCT	CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAG	GACCACTGGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGGGTGGTATTAT	81 GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 	TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCACCATTGCCCAGAAALIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT	GGTTTCTGGCTAGGAGAGCAGCTGGTGCTGGCAAGCAGCACCACCCCTTGGAACATT	TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCA	ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT	TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGTGTTATCATGGAGTGTTTTTTTT	GGCTTCTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTTGCTTTGTTTTTTTT	261 CATGTGCACGATGAGTTCAGGACGGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 	GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT	GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCTGCTGCTCTGTCATGGTGTGTGT	CGCTGCCTCCGCTGCCTCCGCAGCAGCATGATGACTTTGCTGATGACATCTCCTGCTG	501 AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1 	561 CTTTGGTCACAAGTAGGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1	CCACCCACCAAATGCCTCTGCTTGATGGAAAAGGATGGCAAGGTTGGTT

diagnosis of Alzheimer's

the for

The present invention describes a human aspartyl protease I (hu-Aspl)
substrate (I) which comprises a peptide of no more than 50 amino acids,
and which comprises the 8 amino acid sequence Gly-Leu-Ala-Leu-Ala-Leu-Ala-Leu-Ala-Leu-Ala-Leu-Ala-Leu-Ala-Leu-Ala-Leu-Ala-Leu-Ala-Leu-Glu-Pro. Also described are: (I) a method (II) for assaying hu-Aspl
proteolytic activity, comprising: (a) contacting a hu-Aspl protein with
(I) under acidic conditions; and (b) determining the level of hu-Aspl
proteolytic activity; (2) a purified polynuclectide (III) comprising a
nucleotide sequence that hybridises under stringent conditions to the
non-coding strand complementary to a defined 1804 nucleotide sequence
(see ABL22456) where the nucleotide sequence encodes a polypeptide having
confini); (3) a purified polynucleotide (III) (the nucleotide sequence
domain); (3) a purified polynucleotide (III) (the nucleotide sequence
confining to a polypeptide further lacking a pro-peptide domain corresponding
to amino acids 23-62 of hu-Aspl (see ABB78589); (4) a vector (IV)
comprising (III) or (III'); and (5) a host cell (V) transformed or
comprising (III) or (III'); and (5) a host cell (V) transformed or
comprising (III), (III') and/or (IV). The hu-Aspl protease
constraint (III), (III') and herefore diagnose diseases
constraint (III) and herefore diagnose diseases
consequence encodes hu-Aspl expenention. aspartyl protease activity, e.g. 2; 182pp; English. Example 2; Fig 

2070 BP; 476 A; 583 C; 562 G; 449 T; 0 other; Sequence

9 Gaps DB 24; Length 2070; ; 0 0; Indels s; Score 2070; I s; Pred. No. 0; 0; Mismatches Query Match 100.0%; Best Local Similarity 100.0%; Matches 2070; Conservative 0; ò

GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGGCCCGGAGGGGCCAGCTTT GTGGAGATGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC 61 121 121 181 61 g ŏ g ò g

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GGGCTGGCCTATGCTGAGACTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTGACTCT 541

1020 1020 1080 1140 720 720 780 780 840 900 900 960 960 CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGTGGTGCTGCTTTC GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGAGTGGTATTAT GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG TACAACTATGACAAGAGCATTGTGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAA GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT GTGTTTGAAGCTGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT GGTTTCTGGCTAGGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATT ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCCACGTCCCAAGACGACTGT 1081 541 601 661 661 721 781 781 841 841 901 961 1021 1021 601 721 901 961 g g g QQ ò qq ò QQ ò g ŏ q õ 9 ò à Qγ δ

1500 1500 1560 1620 CGCTGCCTCCGCTGCCTGCGCCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1441 1501 1441 1501 1561 1561 a qq ôγ ò ò

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activity. A beta-secretase modulator from the present invention can be used for inhibiting beta-secretase activity in vivo, and in the manufacture of a medicament for the treatment of Alzheimer's disease. Pharmaceutical compositions from the present invention can be used for treating a disease or condition characterised by an abnormal beta-secretase activity. (I) is useful for identifying agents that modulate the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as a core structure to construct derivatives. ABL49914 to ABL49925 and ABB06409 to ABB06593 represent sequences used in the exemplification
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                                                                                                                  the present invention.
                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 2070; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzyme; cleavage site; amyloid protein precursor; APP;
ie; neuroprotective; nootropic; beta-secretase inhibitor;
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                                                                                                                                                                                                                               GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAGG
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                  GGACTGTACCTGTAGGAAACAGAAAAGAAGAAGAAGAAGCACTCTGCTGGCGGGAATACT
                                                                   CTTGGTCACCTCAAATTTAAGTCGGGAAATTCTGCTGGTTGAAACTTCAGCCCTGAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel substrates for human aspartyl protease useful for identifying modulators of beta secretase activity of aspartyl protease for trea? Alzheimer's disease
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Alzheimer's disease; gene; ds.
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12-MAR-2001; 2001US-275251P.
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son RL;
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P-PSDB; ABB06409.
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Heinrikson R
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peptide; disease;

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The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
                                           Purified beta-secretase protein used in assays to discover inhibitors which can be used for the treatment of amyloidogenic diseases e.g.
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                                                                                                                                                                                                                                        Beta-secretase; beta-amyloid precursor protein; beta-amyloid amyloid plaque component; Alzheimer's disease; amyloidogenic
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                                                                                                                                                                                                                     human beta-secretase enzyme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence encodes a human beta-secretase enzyme
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Wang S, McConloque L;
                                                                           ATTAAAAAAAAAAAAAAAAAAAAAAA 2070
                                                                                      Score 2047.8;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                     DNA clone pCEK C1.27 encoding a
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99US-0139172
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Matches 2052; Conservative
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15-JUN-1999;
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GGCACCCAGGCATCCGGCTGCCCTGCGCAGCGGCCTGGGGGGCGCCCCCTGGGG   CTGCGGCTGCCCGGGAGACGCGAGGGCCGGCGGCGGCGGCGCGCGGGGGG	1915 GTGGGCAGCCCCCGCAGACGCTCAACATCCTGGGATACAGGCAGCAGTAACTTTGCA 1974     301 GTGGGTGCTGCCCCCACCCCTTCCTGCATCGTACTACCAGAGGCAGCTGTCCACCACACACA	GCTGGCATCACTGAATCAGACAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG	CCCCTAACCAGTCTGAAGTGCTGGCTGTGGAGGGAGGAGGATGATGTGGAGTATC   CCCCTAACCAGTCTGAAGTGCTGGCCTCTTGGAGGGAGATGATGATGATGTTGGAGGTATC   CCCTCAACCAGTCTGAAGTGCTGGCCTCTTGGAGGAGGAGATGATGGAGGTATC   CCCTCAACCAGTCTGAAGTGCTGGCTGTTGGAGGATGATGATGGAGGTATTATTATCTGCAACTGGAGGAGTGGTAAAAAAGGAGGAGTGGTAAAAAAAGGAGG	1 TACAACTATGACAAGAGCATTGTGGCACCACCACCAACCTTGGTTTGCCCAAGAAA 1 TACAACTATGACAAGAGCATTGTGGACAGTGGCCACCACCAACCTTGGTTTGCCCAAGAAA 1 TACAACTATGACAAGAGCAGCAGTGGGCACCACCACCATTGCCCAAGAAA 1 GTGTTTGAAGCTGCAAATCCATCAAGCAGCACCTCCTCGTTTGCCCAGAAA 1 GTGTTTGAAGCTGCAAATCCATCAAGCAGCACCTCCACGAGAAATTCCTGAT 1 GTTTTGAAGCTGCAAATCCATCAAGCAGCCTCCTCCACGAGAAGTTCCCTGAT 2 GGTTTCTGGCTAGGAGCAGCTGTGGTGCTGGCAGCCACCCCCTGGAAGTTCTGGAAGTTCCTGAT 1 GGTTTCTGGCTAGGAGCAGCTGGTGCTGGCAGCCACCCCCTTGGAACTTTTTTTT	1021 TFCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCA
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                                                                  CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGGTGCTGGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a beta-secretase enzyme. The enzyme cleaves beta-amyloid precursor protein to produce beta-amyloid peptide. This enzyme is therefore implicated in the production of amyloid plaque components which accumulate in the brains of individuals afflicted with Alzheimer's disease. Inhibitors of beta-secretase are administered to a mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-like pathology to test if they maintain or improve cognitive ability or reduce the plaque burden. The compounds are used for the treatment of amyloidogenic diseases e.g. Alzheimer's disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGGTGCTGCCCCCCCTCCTGCATCGCTACCAGAGGCAGCTGTCCAGCACA
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                                                                                                                                                                                                                                                                                                                                                       etase protein used in assays to discover inhibitors for the treatment of amyloidogenic diseases e.g.
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plaque component; Alzheimer's disease; amyloidogenic
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                                                                                                                                                                                                                                                                            John V,
nlogue L;
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ung J, Wang S, McConlogue
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Pred. No. 0;
0; Mismatches
                                                                                                     "beta-secretase"
                                                            Location/Qualifiers
306.1811
/*tag= a
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                                                                                                                                                                                                                                                                                        Tung J,
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Best Local Similarity 99.9%;
Matches 2041; Conservative
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Sinha S, Tatsuno
                                                                                                                               WO200047618-A2.
           inhibitor; ss
                                      Homo sapiens
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       GTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCCAGAAG
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                                                                                                                     GGACTGTACCTGTAGGAAACAGAAAGAGAAGAAGAAGAAGCACTCTGCTGGCGGGAATACT
                                                                                                                              CITGGICACCICAAAITIAAGICGGGAAAITCIGCIGCITGAAACITCAGCCCIGAACCI
                                                                                                                                                                                TTGTCCACCATTCCTTTAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAA
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                             AAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA
                                                          CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCCAGAGCACCTCAGGACCCTCC
                                                                                                                                                                                       Nucleotide sequence of human ASP2 (aspartic protease 2)
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                                                                                                                                                                                                                           This is the nucleotide sequence of the human ASP2 (aspartic protease 2) used in the method of the invention. Agonists and antagonists for ASP2 immunospecific antibodies are used to treat conditions requiring increased or decreased activity or expression of ASP2 respectively. ASP2 is used to treat and diagnose e.g. Alzheimer's disease, cancer and prohormone processing and ASP2 or a fragment can be used to induce an immune response against the above conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTT
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                                                                                                                              New nucleic acid encoding human aspartic protease 2 - used to treat, prevent and diagnose e.g. Alzheimer's disease, cancer and prohormone
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                                                                                                                                                                                                                                                                                                                                                                                             DB 19;
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                                                Smith TS;
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                                                  Ω,
                                                                                                                                                                                                 6-7; 26pp; English.
BEECHAM CORP
BEECHAM PLC.
                                                Powell
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Best Local Similarity 99.5%;
Matches 2049; Conservative
                                                Murphy K,
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1800 1859 1860 1919 1920 1979 1980 2039 2040

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1860 AGTACTGGCATCACACGCAGGTTACCTTGGCGTGTGTCCCTGTGGTACCCTGGCAGAAA
                                                                                                   GAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTAT
                                                                                                                                     TTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTG
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                                                                                                                                                                        AATTAAAAAAAAAAAAAA 2059
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2000US-0177836.
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to an inhibitor t protein; The present sequence is given in a specification relating to an inhibito of catalytically active memapsin 2. The inhibitor binds to the memapsin active site, which is defined by the presence of two catalytic aspartic residues and a substrate binding cleft. The inhibitor is useful for the treatment and diagnosis of Albeimer's disease. It is useful in screens for individuals with a genetic predisposition to Alzheimer's disease. The inhibitor is useful as a reagent for specifically binding to 2 used Novel memapsin 2 inhibitors which bind to active site of memapsin 2 having 2 catalytic aspartic residues and substrate binding cleft, uto treat Alzheimer's disease by blocking amyloid precursor protein precursor amyloid 2; nootropic; neuroprotective; amylinhibitor; Alzheimer's disease; ds.

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                                                                                                                                                                                                                                                                                                                                                                                   Human; memapsin 2; beta secretase; aspartic protease; APP; beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease; neuroprotective; nootropic; expressed sequence tag; EST; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to methods for the production of purified, recombinant catalytically active, memapsin 2 (beta secretase). Memapsin 2, a member of the asparitic protease family, cleaves beta-amyloid precursor protein (APP) found in amyloid plaques. The recombinant memapsin 2 is useful for identifying inhibitors of memapsin 2 in the design of drugs for the treatment and/or prevention of Alzheimer's disease. The recombinant memapsin 2 can be used to immunise against Alzheimer's disease. The present sequence encodes human memapsin 2.
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Human; cytostatic; osteopathic; gynaecological; neuroprotective; antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV; vasotropic; antiarteriosclerotic; antiinfammatory; dermatological; antiarteriosclerotic; antiinfammatory; dermatological; antioralism; antiinfertility; cardiovascular; anticogulant; antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant; antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant; gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic; contraceptive; vaccine; generative disease; multiple solerosis; dystonia; endometriosis; degenerative disease; multiple solerosis; glaucoma; inflammation; skin disorder; obesity; muscular dystrophy; AIDS; infertility; cardiovascular disease; coagulation disease; hypertension;
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                                                                               TGTGGTACCCTGGCAGAGAGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGA
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                                                                                                                                                                                                                                                        diabetes; anxiety; depression; schizophrenia.
gastric ulcer; Alzheimer's disease; gene; ss
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2000IL-0140354.
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GGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACC
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ABL3961 to ABL39818 represent novel human nucleic acid sequences encoding the proteins given in ABB06037 to ABB06164. The novel sequences (NS) can have eyeostatic, osteopathic, gynaecological, neuroprotective, antirheumatic, antiarthritic, antiposorialic, ophthalmological, virucide, vasotropic, antiarthritic, antiinflammatory, dermatological, anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant, immunomodularor, anticonvulsant, antidiabetic, tranquilliser, antiuleer, antidepressant, gastrointestinal, aeuroleptic, cerebroprotective, notropic and contraoptive activities. The NS can be used in vaccines, gene therapy and antisense therapy. Nucleic acids, expression vectors and antibodies from the present invention can be used for treating and isseases, dystonia, multiple sclerosis, inflammation, skin disorders, clasease, dystonia, multiple sclerosis, inflammation, skin disorders, glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular disease, coagulation disease, ischeemia, hypertension, asthma, immune disease, epilepsy, anglaa, neurodegeneration, diabetes, anxiety, antibutical disease, gastric ulcers, stroke, ----CTTTGTGGTGCTGGCTTC 1039 and 120 180 240 300 360 420 874 480 540 009 574 634 694 934 994 514 754 09 GTGGGTGCTGCCCCCCCCCCTGCTGCTGCTGCTACCAGAGGCAGCTGTCCAGCACA GTGGAGATGGTGGACACCTGAGGGCCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG GGCACCCAGCACGGCATCCGGCTGCCCCTGCGCAGCGGCCTGGGGGGGCGCCCCCTGGGG GTGGAGATGGTGGACCAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACC GTGGGCAGCCCCCCCCCCAGACCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCA GTGGGTGCTGCCCCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCACA TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG CTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCACCTTTGTGGTGCTGGTTCT Gaps 75; Length 5757 Sequence 5757 BP; 1485 A; 1490 C; 1392 G; 1388 T; 2 other; 3; Indels DB 24; Score 1894.2; Pred. No. 0; 0; Mismatches Alzheimer's disease and as a contraceptive. 124-126; 290pp; English GGCTGGCCTATGCTGAGATTGCCAGG-91.5%; 96.2%; Query Match Best Local Similarity 96.2° Matches 1981; Conservative 515 575 635 695 755 361 481 935 541 995 455 121 181 301 421 61 601 Claim g δ g δλ a ò g οy qq δy ρp ò q QY g ò Q ò ò

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## SUMMARIES

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Description	Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 2, Appli Sequence 5, Appli
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Score	2070 2070 2070 2070 2070 2070 2070 2070
Result No.	110 8 8 9 9 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Sequence 5, Appli Sequence 5, Appli Sequence 3, Appli Sequence 3, Appli Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 7, Appli Sequence 103, Appl Sequence 103, Appl Sequence 103, Appl Sequence 29, Appl
10 US-09-794-748-5 10 US-09-794-748-5 10 US-09-794-925-5 10 US-09-9681-442-5 10 US-09-968-671A-3 9 US-10-308-365-3 9 US-09-924-340-23 9 US-10-000-986-23 9 US-10-000-986-23 10 US-09-986-34-14-7 10 US-09-794-927-7 10 US-09-794-927-7 10 US-09-794-925-7 10 US-09-794-925-7 10 US-09-794-925-7 10 US-09-794-928-7 10 US-09-794-928-7 10 US-09-917-800A-1665-9 10 US-09-917-800A-1665-9 10 US-09-917-800A-1665-9 10 US-09-917-800A-1665-9 10 US-09-794-414-29 10 US-09-794-827-29 11 US-09-794-827-29 12 US-09-794-827-29 13 US-09-794-827-29 14 US-09-794-827-29
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## ALIGNMENTS

US-09-869-414-3

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND US
TITLE OF INVENTION: THEREFOR
FILE REPERENCE: 2841/6280M
CURRENT APPLICATION NUMBER: US/09/869,414
CURRENT APPLICATION NUMBER: US/09/869,414
CURRENT FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-09-23
PRIOR PLING DATE: 1999-09-23
PRIOR PLING DATE: 1999-09-24
NHOR FILING DATE: 1999-09-24
NHOR FILING DATE: 1999-09-24
NHOR FILING DATE: 1999-09-24
NHOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
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; Sequence 3, Application US/09869444; Publication No. US20030077226A1
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Best Local Similarity 100.
Matches 2070; Conservative
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	TACAACTAIGACAAGACATIGGACAGTGGCACCACCACACTTGGTTGCCCAAGAA 90 INI	QY 1921 AGACCAAGCTTCCCTGCTGGCCAAAGTCAGTAGGAGGATGCACAGTTGCTATT	TTTGCTATT 1980                  TTGCTATT 1980
	GTGTTTGAAGCTGCAGTCAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT 	QY 1981 TGCTTTAGAGACAGGGACTGTATAAACCAAGCGTAACATTGGTGCAAAGATTGCCTCTTGA	SCCTCTTGA 2040
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	1021 TTCCCAGTCATCTCACTCTAATGGGTGAGGTTACCAACCA	RESULT 2 US-09-548-366-3 ; Sequence 3, Application US/09548365	
	1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT 1140 	; PUDICATION NO. USZUJSTU4385AI ; GENERAL INFORMATOY, Mark E. ; APPLICANT: Gurney, Mark E. ; APPLICANT: Bienkowski, Michael J.	
	1141 TACAAGTTTGCCATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAG 1200 	; APPLICANT: Heintikson, Kobert L. ; APPLICANT: Parodi, Luis A. ; APPLICANT: Yan, Kiqiang ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBS'	RATES THEREFOR, AND
	1201 GGCTTCTACGTTGTCTTTGATCGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGC 1260	; TITLE OF INVENTION: USES THEREFOR ; FILE REFERENCE: 28341/6280A ; CURRENT APPLICATION NUMBER: US/09/548,366	

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CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/15,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATCHIN Ver 2.0
SEQ ID NO 3
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US-09-548-366-3
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   APPLICATION NUMBER: 60/101,594
FILING DATE: 1998-09-24
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                               Patentin Ver.
                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                        Similarity
 PRIOR APPLICATION PRIOR FILING DATE:
NUMBER OF SEQ ID NG SOFTWARE: PatentI
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Batent No. US20010018208AI
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Heinrikson, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECF
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 2831/6280DE
CURRENT APPLICATION NUMBER: 09/416,901
PRIOR PLILNG DATE: 1999-10-13
PRIOR FILING DATE: 1999-09-23
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APPLICANT: Bienkowski, Michael J.
APPLICANT: Bienkowski, Michael J.
APPLICANT: Benirkson, Robert L.
APPLICANT: Barodi, Luis A.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECH
TITLE OF INVENTION: THERRECR
TITLE OF INVENTION: THERRECR
TITLE OF INVENTION: THERRECR
TITLE OF INVENTION: THERRECR
TITLE OF INVENTION: UNBER: US/09/794,743
CURRENT APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 73
SOOTWARE: PATENTIN VET: 2.0
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100.0%; Pred. No. 0;
Live 0; Mismatches
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361 TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCCAGGCCAAGTGGGAAGGGGAG   420   421 CTGGGCACCTGCGAAGGGCAGCTGCCAAGTGCCAAGTGCGAAGGGGAG   420   421 CTGGGCACCTGGTGCTGCGTGCCTACTGCAACTT   480   421 CTGGGCACCTGGTGCTGCGTGCCTGTGCTGTGTTT   480   481 GCTGCATCACTGAACTGCAACTGCGAAGATT   480   481 GCTGCATCACTGAACTGAACTGCCAACTGGCAAGTGTTTT   480   481 GCTGCATCACTGAACTGAAGAAGTTCTTCATCAACTGGCAACTGGCAAGTGTTTT   480   481 GCTGCCATCACTGAACTACTACACGGCTCCCAACTGGGAAGCATTCTT   480   481 GCTGCCATCACTGAACTACTCATCATCATCAACGGCTCCCAACTGGAAGGCATCTTG   540   541 GGGCTGGCCTTTGTACTATCATCAACGGCTGACGCTCCCAACTGGAAGCATTCTTGAGTTCTT   600   601 CTGGTAAAGCAACACCACTGAAGCTTCTCCCTGCAACTTTTTTTT	GAGGTCATCATTGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG	1021 TTCCCAGTCATCTCACTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCAC 1080 1021 TTCCCAGTCATCTCACTCAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC 1080 1021 TTCCCAGTCATCTCACTCTAATGGGTGAGGTTACCAACCA

; ORGANISM: US-09-794-74E	SM: Homo sapiens 148-3	qq	61 GGTTTCTGGCTAGGAGCAGCTGGTGTGCTGGCAAGCAGCACCACCCCTTGGAACATT 102
Query Mat Best Loca Matches 2	y Match 100.0%; Score 2070; DB 10; Length 2070; Local Similarity 100.0%; Pred. No. 0; Indels 0; Gaps 0;	Qy	108
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	GTGGGTGCTGCCCCCCCCCCCTTCCTGCATCGTACTACCAGAGCCAGCTGTCCACAGAGCCACCCCACCCCACCCCACACAGAGCCAGCAG	Qy	1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGT
	GIGGGICCIGCCCCCCACCCCTICCIGCATCGCTACCAGAGGCAGCTGTCCAGCACA 30  TACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCGGGCAAGTGGGAAGGGGAG 42	. Qy	1441 CGCTGCCTCCGCTGCCCCGCCAGCAGCATGACTTTGCTGATGACATCTCCCTGCTG 1500
	TACCGGGAACCTCCGGAAGGGTGTGTGTGCCCTACACCCCAGGGCAAGTGGGAAGGGGA 4.2 CTGGGCACCGACGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGC	Qy	1501 AAGTGAGGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
	CTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGC	Qy	1561 CTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAGCACCTCAGGACCCTCC 1620 
	GGTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCTGC 34 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACGACCTTGTTTGACTCT 60	Qy	1621 CCACCCACCAAATGCCTCTGCTTCATGGAGAAGGAAAAGGCTGGCAAGGTGCGTTCCAG 1680 
oy o	<b>u</b> 0 – 0	Qy	1681 GGACTGTACCTGTAGGAAACAGAAAGAAGAAGAAGACACTCTGCTGGCGGGAATACT 1740 
٠ م م	CCCCTCAACCCACGTCCCAACGTCTCTCCCCGGACCTTGGGGGCGCGCGGGGCCTCCTCCCCCCCC	Qy Dp	1741 CITGGICACCTCAAAITTAAGICGGGAAAITCIGCTGCTTGAAACTICAGCCCTGAACCT 1800 1741 CITGGICACCTCAAAITTAAGICGGGAAAITCTGCTGCTTGAAACTICAGCCCTGAACCT 1800
	GACCACTCGCTGTACACAGCAGTCTCTGGTATACACCCATCGGCGGGGGGGG	oy Db.	FFCFFFFCF9              FFCFFFFCF9
	GACCACIICACIGIACACAGGGGGGGGGGGGGGGGGGGG	Qy Db	1861 GTACTGGCATCACGCAGGTTACCTTGGCGTGTGCCTGTGGTACCTGGCAGAGG 1920
80 O	AGGAG 84 AGAAA 90 AGAAA 90	Qy Db	rT 198
	GIGTTTGAAGCIGCAGTCAAATCCAICAAGGCGCCTCCTCCACGGGGAGAAGTTCCCTGAT	Oy Db	1981 TGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGA 2040 
	GCTTTCTGGCGAGCAGCAGCTCAAGCAGCCTCCTCCTCCGAGGAGATCCCTGGT 30	Qy	2041 ATTAAAAAAAAAAAAAAAAAAAAA 2070 

		qq	481 GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG 540
RESULT 7 US-09-794-925-3 : Sequence 3, A	-925-3 e 3. Application US/0979402	Š Š	541 GGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGAGCCTTTCTTT
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; TITLE (	3 X	gg D	61 CCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAG
CURRENT CURRENT CURRENT	FILE REFERENCE: 2841/6280HI CURRENT APPLICATION NUMBER: US/09/794,925 CURRENT FILLIG DATE: 2001-02-27	Qy Dp	721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGGGGAGTGGTATTAT 780
PRIOR F	AFFLICATION NUMBER: 09/410,501 FILING DATE: 1999-10-13 APPLICATION NUMBER: 60/155,493 FITING DAME: 1980-00-12	δ t	1 GAGGTCATCATGTGCGGGTGGAGATCAATGGACAGGATCTGAAAATGGACTGCAAGGAG 84
PRIOR	APPLICATION NE	a d	81 GAGGICAICAITGIGCGGGIGGAGAICAATGGACAGGAICTGAAAATGGACTGCAAGGGG 8
PRIOR F	APPLICATION NU FILING DATE:	à đ	841 TACAACTATGACAAGAACATTGTGGACACGCCACCACCATCCTTTGCCCAAGAA 900  1111111111111111111111111111111111
	ING DATE: 1998-09 SEQ ID NOS: 73 PatentIn Ver. 2.	yo da	901 GTGTTTGAAGCTGCAGTCAATCCATCAAGGCAGCCTCCTCCACGGAAAGTTCCCTGAT 960
; SEQ ID NO 3 ; LENGTH: 20	NO 3 H: 2070 Diva	VO	GGTTTCTGGCTAGGAGGAGCTGGTGTGCTGGCAAGCAGGAGCACCCCTTGGAACATT 1
; ORGANISM: H US-09-794-925-3	ONGANISM: Homo sapiens 9-794-925-3	qq	961 GGTTTCTGGCTAGGAGAGCAGCTGGTGGTGGTGGTGGAGCAGCCACCCCTTGGAACATT 1020
1	100.0%; Score 2070; DB 10; Length 2070; milarity 100.0%; Pred. No. 0;	Oy Dp	1021 TTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTACCAACCA
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oy da	GTGGGGGTGCCCGGGGGGGGGGGGGGGGGGCCGGGCCG	Qy Db	1261 CATGTGCACGATGAGTTCAGGACGGCAGGGGGGGGGGCCTTTTGTCACCTTGGACATG 1320 
3 & E	GTGGGCAGCCCCCCCCGCAGACACACACACGCGCAGGCACAGGCACACGGCAGCA	Qy	1321 GAAGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTAT 1380 
g vo e	GEORGE   G	Qy Dp	1381 GTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTGT
S & E	TACCGGACCTCCGGAAGGGTGTATGTGCCCTACACGGGCAAGTGGCAAGGGGAGGGGGAGGAGGGGGAGGGGGAGGGGGGAGGGGG	Qy	1441 CGCTGCCTCCCTGCCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGCTG 1500
g & d	TACCGGGCCCCGGTANGGGGGGGGGGGGGGGGGGGGGGGG	QY	1501 AAGTGAGGAGCCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCA 1560
oy 53	GCTGCCATCACTGAATCAGAAGTTCTTCATCAACGCTCCAACTGGGGAAGGCATCCTG  GCTGCCATCACTGAATCATCATCAACGGCTCCAACTGGGAAGGCATCCTG  IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy Dp	1561 CTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCCAGAGCACCTCAGGACCCTCC 1620 

1 ATGGCCCAAGCCCTGCCTGCTGTGGATGGGCGGGGAGTGCTGCCTGC	41 GTGGGGAGCCCCCGCAGAGCCTCAACATCTGGTGGTACAGCACCAGTAACTTTGCA 3   1   1   1   1   1   1   1   1   1	61 TACCGGGACCTCCGGAAGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAG 42 [	481 GCTGCATCATGAATCAGAAGATTCATCAACGAGTGGAAGGGCATCCTG 540	601 CTGGTAAAGCACCCACGTTCCCAACCTTCTCCCTGCACCTTTGTGGTGCTTC 660	721 GACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGGCGGGAGTGGTATTAT 780	841 TACAACTATGACAAGACATTGTGGACAGTGGCACCACCAACTTGGTTTGCCCAAGAAA 900	61 61 21 21 81	TTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCCACGTCCCAAGACGACT
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	Oy . 1801 TTGTCCACCATTCCTTTAAATTCTCCAACCCAAGTATTCTTTCT	HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 2041 ATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	; GENERAL IMFORMATION: ; APPLICANT: Gurney, Mark E. ; APPLICANT: Bienkowski, Michael J. ; APPLICANT: Bienkowski, Michael J. ; APPLICANT: Parodi, Luis A. ; APPLICANT: Yan, Riquing ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES ; TITLE OF INVENTION: THEREFOR	; FILE REFERENCE: 28341/6280FG ; CURRENT APPLICATION NUMBER: US/09/681,442 CURRENT FILING DATE: 2001-04-05 PRIOR APPLICATION NUMBER: 09/416,901 ; PRIOR PILING DATE: 1999-10-13 ; PRIOR APPLICATION NUMBER: 60/155,493 ; PRIOR FILING DATE: 1999-09-23 ; PRIOR APPLICATION NUMBER: 09/404,133	; PRIOR FILING DATE: 1999-09-23 ; PRIOR APPLICATION UNMBER: PCT/US99/20881 ; PRIOR APPLICATION NUMBER: 60/101,594 ; PRIOR APPLICATION NUMBER: 60/101,594 ; NUMBER OF SEQ ID NOS: 73 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 3	; LENGTH: 2070 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-681-442-3 Query Match Best Local Similarity 100.0%; Score 2070; DB 10; Length 2070; Matches 2070; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 ATGGCCCAAGCCCTGCCTGCTGTGGATGGGCGGGGAGTGCTGCCTGC	

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GCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGGGAAGGCATCCTG
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: LOCATION: (2455)(2456)(2463)(2478)(2480)(2497)(2507)(2509)(2512)(2516)

: LOCATION: (2520)(2522)(2529)(2539)(2540)

: OTHER INFORMATION: Wherein n can be represented by a, c, t, or g

US-09-969-671A-1
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Pred. No. 0;
0; Mismatches
APPLICANT: POWELL, DAVID J.
TITLE OF INVENTION: ASP2
TITLE REFERENCE: GH-70368-D1
CURRENT PELICATION NUMBER: US/09/969,671A
CURRENT FILING DATE: 2001-10-03
PRIOR PELICATION NUMBER: US/09/969,671A
PRIOR APPLICATION NUMBER: 09/009,191
PRIOR APPLICATION NUMBER: 09/009,191
PRIOR APPLICATION NUMBER: 09/694,200
PRIOR FILING DATE: 1998-01-20
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 1
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Best Local Similarity 99.5%;
Matches 2049; Conservative (
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Sequence 1, Application US/09969671A Publication No. US20030036112A1 GENERAL INFORMATION: APPLICANT: CHAPMAN, CONRAD G. APPLICANT: MURPHY, KAY

Db   1261 CATGTGCACGATGGACGGCGGCGGGGGAGGCCCTTTGTCACGTTGGACATG 1320     Qy	CGCTGCCTCCCGCCGCGCGCGGCGGGGGGGGGGGGGGG	Db   1561 ACTITGGTCACAAGTAGGACACAGATGGCACCTGTGGCCAGAGCACCTC GCO   1620 CCCACCCCACAAATGCTTGCTTGATGAAGAAAGAAGAAGAAGAAGAAGAAGAAGAAGAACAAGAACAAGAACAAGAACAAC		Db 1801 TTTGTCCACATTCTTTAAATTCTCCAACCAAAGTATTCTTTTTTTT	OY 1920 GAGACCAAGCTTGTTTCCCTGCTGCCAAAGTCAGTAGGAGGATGCACAGTTTGCTAT 1979	Oy 2040 AATTAAAAAAAAAA 2059 	RESULT 11 US-09-795-903A-1 ; Sequence 1, Application US/09795903A ; Patent No. US20020164760A1 ; GENERAL INFORMATION: ; APPLICANT: Tang, Jordan J.N. ; APPLICANT: Lin, Xinli	### APPLICANT: Koclsch, Gerald ### TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods ### TITLE OF INVENTION: Of Use Thereof ### FILE REPERBUCE: OMRE' 179 ### APPLICANTON WIMMED: 15,002,003	606	FALOR FILLING DATE: 1999-11.0 () PRIOR FILLING DATE: 1999-11.0 () PRIOR APPLICATION NUMBER: 60/177,836
			Db   601 CTGGTAAAGCAGACCCACGTTCCCAACCTGTCTGCAGCTTTGTGGTGCTGGCTTC 660		OY 841 TACAACTATGACAAGAGCATTGTGGCACCACCAACCAACC	OY 961 GGTTTCTGGCTAGGAGCAGCTGGTGTGCTGGCAAGCAGCACCACCCCTTGGAACATT 1020	Oy         1021 TTCCCAGTCATCTCACTTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC         1080           Db         1021 TTCCCAGTCATCTCACTTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACC         1080           Qy         1081 ATCCTTCCGCAGCAATACCTGCGGCCAGGGAGATGTGGCCACGTCCCAAGACGACTGT         1140           Db         1081 ATCCTTCCGCAGCAATACCTGCGGCCAGGGAGATGTGGCCACGTCCCAAGACGACTGT         1140           Db         1081 ATCCTTCCGCAGCAATACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGT         1140	Oy 1141 TACAAGTTTGCCATCTCACAGGCACTGTTATGGGAGCTGTTATCATGGGG 1200 	Qy     1201 GGCTTCTACGTTGTCTTTGATCGGCCCCGAAACGAATTGCTTTGCTGTCAGCGCTTGC     1260       LILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 1261 CATGTGCACGATGAGTTCAGGACGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATG 1320

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## PRIOR FILING DATE: 2000-01-25   PRIOR APPLICATION NUMBER: 60/178,368   PRIOR FILING DATE: 2000-01-27   PRIOR FILING DATE: 2000-01-27   PRIOR FILING DATE: 2000-06-08   PRIOR FILING DATE: 2000-06-08   NUMBER: OF EXQ ID NOS: 31   SEQ ID NO 1   SEQ ID NO 1   LENGTH: 3252   TYPE: DAA	Query Match  97.1%; Score 2010; DB 9; Length 3252;  Best Local Similarity 99.8%; Pred. No. 0;  Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  Qy 40 GCGGGAGTGCTGCCTACGCACGCACGGCATCCGGCTGCCCTGCGCAGCGC 99  [	100 CTGGGGGGCCCCCCTGGGGCTGGGCTGCCCCGGGAGCCGAGGGGGGGG	DD	280 ACAGGCAGCAGTAACTTTGCAGTGGTGCCCCCCCCCCCC	Db   301 CAGAGGCAGCTGTCCAGCACATACCGGGAGCTCTCCGGAAGGGTGTGTGT	460 GTCACTGTGCGTQCCAACATTGCTGCCATCACTGAATCAGACAACTTCTTCATCAACGGC 5   1111111111111111111111111111111111	1	640 CACCTTGGGGCTGCCTCCCCCTCAACCAGTCCCCAACTCTGTGCGGGGGGGG	OY 700 AGCATGATCATTGGAGGTATCGACCACTGGTGTACACAGGCACTCTCTGGTATACACCC 759	Db 721 ATCCGGGGGGGGTATTATGTGGTGATTGTGGGGGGGGGG

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                                 APPLICANT: Tang, Jordan J.N.
APPLICANT: Koelsch, Gerald
APPLICANT: Koelsch, Gerald
APPLICANT: Ghosh, Arun K.
TITLE OF INVENTION: Inhibitors of Memapsin 2 and
FILE REPERBKCE: 2932.1006-007
CURRENT APPLICATION NUMBER: US/10/032,818
CURRENT FILING DATE: 2001-12-28
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Pred. No. 0;
0; Mismatches
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PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/258,705
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                               Sequence 1, Application US/10032818 Publication No. US20030092629A1 GENERAL INFORMATION:
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DD	Db   1801 CTTCTTTCTTAGTTTCAGAAGTACTGGCATCACGCAGGTTACCTTGGCGTGTCCC 1860     Qy		GENERAL INFORMATION: APPLICANT: Tang, Jordan J.N. APPLICANT: Tang, Jordan J.N. TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods TITLE OF INVENTION: of Use Thereof FILE REFERENCE: OMRF 179 CURRENT FILING DATE: 2001-02-28 CURRENT PAPLICATION NUMBER: 09/604.608	. ω	; ORGANISM: Homo sapiens US-09-796-264-1  Query Match 97.1%; Score 2010; DB 10; Length 3252; Best Local Similarity 99.8%; Pred. No. 0; Matches 2013; Conservative 0; Mismatches 5; Indels 0; Gaps 0; A GGGGAGTGCTGCCCGCCACGCACCCAGCGCTCCGCCTGCGCAGCGC 9

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 APPLICATION NUMBER: 60/210,292
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-00;
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2
SEQ ID NO 1
                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                  Best Local Similarity
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Patent No. US20020115600A1
GENERAL INFORMATION:
APPLICANT: Tang, Jordan J.N.
APPLICANT: Hong, Lin
TITLE OF INVENTION: Inhibitors of Memapsin 2 and
FILE REFERENCE: OMRF 182
CURRENT APPLICATION NUMBER: US/09/845,226
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: 09/603,713
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR FILING DATE: 2000-01-25

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